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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/226,046

DATE: 08/06/1999  
TIME: 15:41:04

Input Set: I226046.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Reppert, Steven M.
2      Ebisawa, Takashi
3  <120> TITLE OF INVENTION: HIGH-AFFINITY MELATONIN RECEPTOR AND USES THEREOF
4  <130> FILE REFERENCE: 10217/250003
5  <140> CURRENT APPLICATION NUMBER: US/09/226,046
6  <141> CURRENT FILING DATE: 1999-01-05
7  <150> EARLIER APPLICATION NUMBER: US 08/466,103
8  <151> EARLIER FILING DATE: 1995-06-06
9  <150> EARLIER APPLICATION NUMBER: US 08/319,887
10 <151> EARLIER FILING DATE: 1994-10-07
11 <150> EARLIER APPLICATION NUMBER: US 08/261,857
12 <151> EARLIER FILING DATE: 1994-06-17
13 <160> NUMBER OF SEQ ID NOS: 29
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
15 <210> SEQ ID NO 1
16 <211> LENGTH: 1320
17 <212> TYPE: DNA
18 <213> ORGANISM: Xenopus laevis
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (32)...(1291)
22 <400> SEQUENCE: 1
23      tgcctatctc cctttgccag ggggcagaga a atg atg gag gtg aat agc act      52
24                                     Met Met Glu Val Asn Ser Thr
25                                     1           5
26      tgc ttg gat tgc agg aca cct ggt acc ata cga aca gag cag gat gca      100
27      Cys Leu Asp Cys Arg Thr Pro Gly Thr Ile Arg Thr Glu Gln Asp Ala
28          10           15           20
29      cag gac agc gca tct cag gga ctc acc tct gcc ctg gcg gtg gtt ctt      148
30      Gln Asp Ser Ala Ser Gln Gly Leu Thr Ser Ala Leu Ala Val Val Leu
31          25           30           35
32      ata ttc acc att gtt gtg gat gtc ctg ggc aat ata ttg gtc att ttg      196
33      Ile Phe Thr Ile Val Val Asp Val Leu Gly Asn Ile Leu Val Ile Leu
34          40           45           50           55
35      tct gtc ctg agg aac aag aag ctg cag aat gct gga aat ctc ttt gtt      244
36      Ser Val Leu Arg Asn Lys Lys Leu Gln Asn Ala Gly Asn Leu Phe Val
37          60           65           70
38      gtc agt ttg tct att gcc gat ctg gtt gtt gct gtg tat ccc tat ccg      292
39      Val Ser Leu Ser Ile Ala Asp Leu Val Val Ala Val Tyr Pro Tyr Pro
40          75           80           85
41      gtc att ctc ata gct att ttc cag aat gga tgg acg ctt gga aat atc      340
42      Val Ile Leu Ile Ala Ile Phe Gln Asn Gly Trp Thr Leu Gly Asn Ile
43          90           95           100
44      cat tgt cag atc agt ggc ttc ctg atg gga ctc agc gtt att gga tca      388

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45	His Cys Gln Ile Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser	
46	105 110 115	
47	gtc ttc aac ata aca gcc ata gct atc aac agg tat tgc tac atc tgc	436
48	Val Phe Asn Ile Thr Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys	
49	120 125 130 135	
50	cac agc ctg aga tat gac aag ctt tat aat caa aga agc acc tgg tgc	484
51	His Ser Leu Arg Tyr Asp Lys Leu Tyr Asn Gln Arg Ser Thr Trp Cys	
52	140 145 150	
53	tac ctt ggc ctg aca tgg ata cta act ata att gca atc gtg cca aac	532
54	Tyr Leu Gly Leu Thr Trp Ile Leu Thr Ile Ile Ala Ile Val Pro Asn	
55	155 160 165	
56	ttt ttt gtt gga tca cta cag tat gac ccc agg att ttt tct tgc aca	580
57	Phe Phe Val Gly Ser Leu Gln Tyr Asp Pro Arg Ile Phe Ser Cys Thr	
58	170 175 180	
59	ttt gcg cag aca gtg agt tcc tca tac acc ata aca gta gtg gtg gtg	628
60	Phe Ala Gln Thr Val Ser Ser Ser Tyr Thr Ile Thr Val Val Val Val	
61	185 190 195	
62	cat ttt ata gtc cct ctt agt gtt gtg aca ttc tgt tac tta aga ata	676
63	His Phe Ile Val Pro Leu Ser Val Val Thr Phe Cys Tyr Leu Arg Ile	
64	200 205 210 215	
65	tgg gtt tta gtg atc caa gtc aaa cac aga gtt aga caa gac ttc aag	724
66	Trp Val Leu Val Ile Gln Val Lys His Arg Val Arg Gln Asp Phe Lys	
67	220 225 230	
68	caa aag ttg aca caa aca gac ttg aga aat ttc ttg acc atg ttt gtg	772
69	Gln Lys Leu Thr Gln Thr Asp Leu Arg Asn Phe Leu Thr Met Phe Val	
70	235 240 245	
71	gtc ttt gta ctt ttt gca gtt tgc tgg gcc ccc tta aac ttt atc ggc	820
72	Val Phe Val Leu Phe Ala Val Cys Trp Ala Pro Leu Asn Phe Ile Gly	
73	250 255 260	
74	ctt gct gtg gcc att aat ccg ttt cat gtg gca cca aag att cca gaa	868
75	Leu Ala Val Ala Ile Asn Pro Phe His Val Ala Pro Lys Ile Pro Glu	
76	265 270 275	
77	tgg ctg ttt gtt tta agc tat ttc atg gcc tat ttt aac agt tgt ctc	916
78	Trp Leu Phe Val Leu Ser Tyr Phe Met Ala Tyr Phe Asn Ser Cys Leu	
79	280 285 290 295	
80	aat gct gtt ata tat ggt gtg cta aat caa aac ttc cgc aag gag tac	964
81	Asn Ala Val Ile Tyr Gly Val Leu Asn Gln Asn Phe Arg Lys Glu Tyr	
82	300 305 310	
83	aaa aga ata ctg atg tcc tta ttg act cca aga ctg ttg ttt ctt gac	1012
84	Lys Arg Ile Leu Met Ser Leu Leu Thr Pro Arg Leu Leu Phe Leu Asp	
85	315 320 325	
86	aca tct aga gga gga act gag gga ttg aaa agt aag cct tcg cca gct	1060
87	Thr Ser Arg Gly Gly Thr Glu Gly Leu Lys Ser Lys Pro Ser Pro Ala	
88	330 335 340	
89	gta acc aac aac aat caa gca gat atg cta gga gaa gca agg tca ctg	1108
90	Val Thr Asn Asn Asn Gln Ala Asp Met Leu Gly Glu Ala Arg Ser Leu	
91	345 350 355	
92	tgg ctg agc agg aga aat ggt gcg aaa atg gtg atc atc atc agg cca	1156
93	Trp Leu Ser Arg Arg Asn Gly Ala Lys Met Val Ile Ile Ile Arg Pro	
94	360 365 370 375	

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105      aga aaa gca caa att gca atc atc cat caa ata ttc tgg cct cag agt      1204
106      Arg Lys Ala Gln Ile Ala Ile Ile His Gln Ile Phe Trp Pro Gln Ser
107              380                      385                      390
108      tca tgg gca aca tgc cgt caa gac aca aag att acc gga gaa gaa gat      1252
109      Ser Trp Ala Thr Cys Arg Gln Asp Thr Lys Ile Thr Gly Glu Glu Asp
110              395                      400                      405
111      ggc tgc cgt gaa ctg tgc aag gac ggg att tcc caa agg tgagacccaa      1301
112      Gly Cys Arg Glu Leu Cys Lys Asp Gly Ile Ser Gln Arg
113              410                      415                      420
114      tgcactatat ccacattat      1320
115      <210> SEQ ID NO 2
116      <211> LENGTH: 420
117      <212> TYPE: PRT
118      <213> ORGANISM: Xenopus laevis
119      <400> SEQUENCE: 2
120      Met Met Glu Val Asn Ser Thr Cys Leu Asp Cys Arg Thr Pro Gly Thr
121              1              5              10              15
122      Ile Arg Thr Glu Gln Asp Ala Gln Asp Ser Ala Ser Gln Gly Leu Thr
123              20              25              30
124      Ser Ala Leu Ala Val Val Leu Ile Phe Thr Ile Val Val Asp Val Leu
125              35              40              45
126      Gly Asn Ile Leu Val Ile Leu Ser Val Leu Arg Asn Lys Lys Leu Gln
127              50              55              60
128      Asn Ala Gly Asn Leu Phe Val Val Ser Leu Ser Ile Ala Asp Leu Val
129              65              70              75              80
130      Val Ala Val Tyr Pro Tyr Pro Val Ile Leu Ile Ala Ile Phe Gln Asn
131              85              90              95
132      Gly Trp Thr Leu Gly Asn Ile His Cys Gln Ile Ser Gly Phe Leu Met
133              100             105             110
134      Gly Leu Ser Val Ile Gly Ser Val Phe Asn Ile Thr Ala Ile Ala Ile
135              115             120             125
136      Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Arg Tyr Asp Lys Leu Tyr
137              130             135             140
138      Asn Gln Arg Ser Thr Trp Cys Tyr Leu Gly Leu Thr Trp Ile Leu Thr
139              145             150             155             160
140      Ile Ile Ala Ile Val Pro Asn Phe Phe Val Gly Ser Leu Gln Tyr Asp
141              165             170             175
142      Pro Arg Ile Phe Ser Cys Thr Phe Ala Gln Thr Val Ser Ser Ser Tyr
143              180             185             190
144      Thr Ile Thr Val Val Val Val His Phe Ile Val Pro Leu Ser Val Val
145              195             200             205
146      Thr Phe Cys Tyr Leu Arg Ile Trp Val Leu Val Ile Gln Val Lys His
147              210             215             220
148      Arg Val Arg Gln Asp Phe Lys Gln Lys Leu Thr Gln Thr Asp Leu Arg
149              225             230             235             240
150      Asn Phe Leu Thr Met Phe Val Val Phe Val Leu Phe Ala Val Cys Trp
151              245             250             255
152      Ala Pro Leu Asn Phe Ile Gly Leu Ala Val Ala Ile Asn Pro Phe His
153              260             265             270
154      Val Ala Pro Lys Ile Pro Glu Trp Leu Phe Val Leu Ser Tyr Phe Met

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145		275		280		285	
146	Ala	Tyr	Phe	Asn	Ser	Cys	Leu
147		290		295		300	
148	Gln	Asn	Phe	Arg	Lys	Glu	Tyr
149		305		310		315	
150	Pro	Arg	Leu	Leu	Phe	Leu	Asp
151				325		330	
152	Lys	Ser	Lys	Pro	Ser	Pro	Ala
153				340		345	
154	Leu	Gly	Glu	Ala	Arg	Ser	Leu
155				355		360	
156	Met	Val	Ile	Ile	Ile	Arg	Pro
157				370		375	
158	Gln	Ile	Phe	Trp	Pro	Gln	Ser
159				385		390	
160	Lys	Ile	Thr	Gly	Glu	Glu	Asp
161					405		410
162	Ile	Ser	Gln	Arg			
163					420		
164	<210> SEQ ID NO 3						
165	<211> LENGTH: 1149						
166	<212> TYPE: DNA						
167	<213> ORGANISM: Ovis						
168	<220> FEATURE:						
169	<221> NAME/KEY: CDS						
170	<222> LOCATION: (49)...(1146)						
171	<400> SEQUENCE: 3						
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173	Met Ala Gly						
174	1						
175	cgg ctg tgg ggc tcg ccg ggc ggg acc ccc aag ggc aac ggc agc agc						
176	Arg Leu Trp Gly Ser Pro Gly Gly Thr Pro Lys Gly Asn Gly Ser Ser						
177	5 10 15						
178	gcg ctg ctc aac gtc tcg cag gcg gcg ccc ggc gcc ggg gac ggt gtg						
179	Ala Leu Leu Asn Val Ser Gln Ala Ala Pro Gly Ala Gly Asp Gly Val						
180	20 25 30 35						
181	cgg ccg cgg ccc tcg tgg ctg gcc gcc acc ctc gcc tcc atc ctc atc						
182	Arg Pro Arg Pro Ser Trp Leu Ala Ala Thr Leu Ala Ser Ile Leu Ile						
183	40 45 50						
184	ttc acc atc gtg gtg gac atc gtg ggc aac ctc ctg gtg gtc ctg tcc						
185	Phe Thr Ile Val Val Asp Ile Val Gly Asn Leu Leu Val Val Leu Ser						
186	55 60 65						
187	gtg tat cgg aac aag aag ctg agg aac gca ggg aat gtg ttt gtg gtg						
188	Val Tyr Arg Asn Lys Lys Leu Arg Asn Ala Gly Asn Val Phe Val Val						
189	70 75 80						
190	agc ctg gca gtt gca gac ctg ctg gtg gcc gtg tat ccg tac ccc ttg						
191	Ser Leu Ala Val Ala Asp Leu Leu Val Ala Val Tyr Pro Tyr Pro Leu						
192	85 90 95						
193	gcg ctg gcg tct ata gtt aac aat ggg tgg agc ctg agc tcc ctg cat						
194	Ala Leu Ala Ser Ile Val Asn Asn Gly Trp Ser Leu Ser Ser Leu His						

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**RAW SEQUENCE LISTING**  
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195	100	105	110	115	
196	tgc	caa	ctt	agt	ggc
197	Cys	Gln	Leu	Ser	Gly
198					
199	ttc	agc	atc	acg	gga
200	Phe	Ser	Ile	Thr	Gly
201					
202	agc	ctc	aga	tac	ggc
203	Ser	Leu	Arg	Tyr	Gly
204					
205	gtg	ttc	ctg	atc	tgg
206	Val	Phe	Leu	Ile	Trp
207					
208	tgt	gtg	ggg	acc	ctg
209	Cys	Val	Gly	Thr	Leu
210					
211	acg	cag	tcc	gtc	agc
212	Thr	Gln	Ser	Val	Ser
213					
214	ttc	ata	ggt	ccg	atg
215	Phe	Ile	Val	Pro	Met
216					
217	gcc	ctg	ggt	ctt	cag
218	Ala	Leu	Val	Leu	Gln
219					
220	aaa	ctg	aag	ccc	cag
221	Lys	Leu	Lys	Pro	Gln
222					
223	ttt	gtc	ctc	ttt	gcc
224	Phe	Val	Leu	Phe	Ala
225					
226	ggt	gtg	gcc	tcg	gac
227	Val	Val	Ala	Ser	Asp
228					
229	ctg	ttt	gtg	gct	agt
230	Leu	Phe	Val	Ala	Ser
231					
232	gcg	atc	ata	tat	gga
233	Ala	Ile	Ile	Tyr	Gly
234					
235	aaa	att	ata	gtc	tca
236	Lys	Ile	Ile	Val	Ser
237					
238	tcc	aat	cat	gta	gca
239	Ser	Asn	His	Val	Ala
240					
241	gcc	aac	cat	aac	cta
242	Ala	Asn	His	Asn	Leu
243					
244					

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I226046.RAW

Line	Error/Warning	Original Text
408	W "N" or "Xaa" used: Feature required	Asn Pro Xaa Xaa Tyr
433	W "N" or "Xaa" used: Feature required	Gly Asn Xaa Phe Val Val
824	W "N" or "Xaa" used: Feature required	Asn Ala Xaa Xaa Tyr